

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: BILLING-MEDEL, PATRICIA A.
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
HAYDEN, MARK
KLASS, MICHAEL R.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
- (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS FOR THE
USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
- (iii) NUMBER OF SEQUENCES: 51
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/828,856
(B) FILING DATE: 31-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441.
(C) REFERENCE/DOCKET NUMBER: 6068.US.P1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 847/935-1729
(B) TELEFAX: 847/938-2623
(C) TELEX:

10025167.121901

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCCAGGAATA	ACTAGAGAGS	AACAATGGGS	TTATTCAGAG	GTTTGTGTTT	CCTCTTAGTT	60
CTGTGCCTGC	TGCACCACTC	AAATACTTCC	TTCATTAAGC	TGAATAATAA	TGGCTTTGAA	120
GATATTGTCA	TGTTTATAGA	TCCTAGTGTG	CCAGAAGATG	AAAAAATAAT	TGAACAAATA	180
GAGGATATGG	TGACTACAGC	TCTACGTAC	CTGTTTGAAG	CCACAGAAAA	AAGATTTTTT	240
T						241

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAGAGAGGA	ACAATGGGGT	TATTCAGAGG	TTTTGTTTTT	CTCTTAGTTC	TGTGCCTGCT	60
GCACCACTCA	AATACTTCCT	TCATTAAGCT	GAATAATAAT	GGCTTTGAAG	ATATTGTCAT	120
TGTTATAGAT	CCTAGTGTGC	CAGAAGATGA	AAAAATAATT	GAACAAATAG	AGGATATGGT	180
GACTACAGCT	TCTACGTACC	TGTTTGAAGC	CACAGAAAA			219

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTNTGTAACG	AAAAAACCCA	TAATCAAGAA	GCTCCAAGCC	TACAAAACAT	AAAGTGCAAT	60
TTTAGAAGTA	CATGGGAGGT	GATTAGCAAT	TCTGAGGATT	TTAAAAACAC	CATACCCATG	120
GTGACACCAC	CTCCTCCACC	TGCTTCTCA	TTGCTGAAGA	TCAGTCAAAG	AATTGTGTGC	180
TTAGTCTTGG	ATAAGTCTGG	AAGCATGGGG	GGTAAGGACC	GCCTAAATCG	A	231

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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TGGGGGGTAA	GGACCGCCTA	AATCGAATGA	ATCAAGCAGC	AAAACATTTC	CTGCTGCAGA	60
CTGTTGAAAA	TGGATCCTGG	GTGGGGATGG	TTCACTTTGA	TAGTACTGCC	ACTATTGTAA	120
ATAAGCTAAT	CCAAATAAAA	AGCAGTGTAT	AAAGAAACAC	ACTCATGGCA	GGATTACSTA	180
CATATCTCT	GGGAGGAAGT	TCCATCTGCT	CTGGAATTAA	ATATGCATT	CAGGTGA	237

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTCCATCTG	CTCTGGAATT	AAATATGCAT	TTCAGGTGAT	TGGAGAGCTA	CATTCCCAAC	60
TCGATGGATC	CGAAGTACTG	CTGCTGACTG	ATGGGGAGGA	TAACACTGCA	AGTTCTTGTA	120
TGTGATGAAT	GAACAAAGT	GGGGCCATTG	TTCATTTTAT	TGCTTTGGGA	AGAGCTGCTG	180
ATGAAGCAGT	AATAGAGATG	AGCAAGATAA	CAGGAG			216

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /note= "N" represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTGATAGT	ACAGTGGGAA	AGGNCAGTT	CTTTCTCATC	ACATGGAACA	GTCTGCCTCC	60
CAGTATTCT	CTCTGGGATC	CCAGTGGAA	AATAATGGAA	AATTTACAG	TGGATGCAAC	120
TTCCAAAATG	GCCTATCTCA	GTAITCCAGG	AACATGCAAG	GTGGGCACIT	GGGCATACAA	180
CTTTCAAGCC	AAAGCGAACC	C				201

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCAAAATCTT	CTGTGCCTCC	AATCACAGTG	AATGCTAAA	TGAATAAGGA	CGTAAACAGT	60
TTCCCCAGCC	CAATGATTGT	TTACGCAGAA	ATTCTACAG	GATATGTACC	TGTTCTTGGA	120
GCCAATGTGA	CTGCTTTTAT	TGAATCACAG	AATGGACATA	CAGAAGTTTT	GGAACITTTG	180
GATAATGGTG	CAGGCGCTGA	TTCTTTCAAG	AATGATGGAG	TCTACTCCAG	GTAITTTTACA	240
G						241

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCAGGCGC	TGATTCTTTC	AAGAATGATG	GAGTCTACTC	CAGGTATTTT	ACAGCATATA	60
CAGAAAATGG	CAGATATAGC	TTAAAAGTTC	GGGCTCATGG	AGGAGCAAAC	ACTGCCAGGC	120
TAAAATTACG	GCCTCCACTG	AATAGAGCGC	CGTACATACC	AGGCTGGGTA	GTGAACGGGG	180
AAATTGAAGC	AAACCCGCCA	AGACCTGAAA	TTGATGAGGA	TACTCAGACC	ACCTTGGAGG	240
AT						242

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGCCAAGA	CCTGAAATTTG	ATGAGGATAC	TCAGACCACC	TTGGAGGATT	TCAGCCGAAC	60
AGCATCCGGA	GGTGCAATTTG	TGGTATCACA	AGTCCCAAGC	CTTCCCTTGC	CTGACCAATA	120
CCCACCAAGT	CRAATCACAG	ACCTTGATGC	CACAGTTTAT	GAGGATAAGA	TTATTCTTAC	180
ATGGACAGCA	CCAGGAGATA	ATTTTGATGT	TGGAAGAGTT	CAACGTTATA	TCA	233

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: base_polymorphism
(B) LOCATION: 22
(D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
(A) NAME/KEY: base_polymorphism
(B) LOCATION: 44
(D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAATACCCA	CCAAGTCAAA	TNACAGACCT	TGATGCCACA	GTINATGAGG	ATAAGATTAT	60
TCTTACATGG	ACAGCACACG	GAGATAATTT	TGATGTTGGA	AAAGTTCAAC	GTTATATCAT	120
AAGAATAAGT	GCAAGTATTC	TTGATCTAAG	AGACAGTTTT	GATGATGCTC	TTCAAGTAAA	180
TACTACTGAT	CTGTACACAA	AGGAGGCCAA	CTCCAAGGAA	AGCTTTGCAT	TTAAACCGA	240
AAATATCTCA	GAAGAAAATG	CAACCCACAT	ATTATTGCGC	ATTAAAAAGTA	TAGATAAAGC	300
ATTTGGCATC	AAA					313

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGTATTCTT	GATCTAAGAG	ACAGTTTGA	TGATGCTCTT	CAAGTAAATA	CTACTGATCT	60
GTCACCAAAG	GAGGCCAACT	CCAAGGAAAG	CTTTGCATT	AAACCAGAAA	ATATCTCAGA	120
AGAAAATGCA	ACCCACATAT	TTATTGCCAT	TAAAGTATA	GATAAAAGCA	ATTTGACATC	180
AAAAGTATCC	AACATTGCAC	AAGTAACITT	GTTTATCCCT	CAAGCAAATC	CTGATGACAT	240
TG						242

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ANANAATGCA	ACCCACATAT	TTATTGCCAT	TAAAGTATA	GATAAAAGCA	ATTTGACATC	60
AAAAGTATCC	AACATTGCAC	AAGTAACITT	GTTTATCCCT	CAAGCAAATC	CTGATGACAT	120
TGATCCTACT	CCTACTCCTA	CTCCTACTCC	TGATAAAAGT	CATAATTCTG	GAGTTAATAT	180
TTCTACGCTG	GTATTGCTG	TGATTGGG				208

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCCTACTCC	TACTCTGAT	AAAAGTCATA	ATTCTGGAGT	TAATATTCT	ACGCTGGTAT	60
TGTCGTGAT	TGGGTCTGTT	GTAATTGTTA	ACTTTATTTT	AAGTACCACC	ATTTGAACCT	120
TAACGAAGAA	AAAAATCTTC	AAGTAGACCT	AGAAGAGAGT	TTTAAAAAAC	AAAACAATGT	180
AAGTAAAGGA	TATTTCIGAA	T				201

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 111
- (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

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- (ix) FEATURE:
 (A) NAME/KEY: base_polymorphism
 (B) LOCATION: 244
 (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
 (A) NAME/KEY: base_polymorphism
 (B) LOCATION: 284
 (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCTGTTGTA	TTGTTAACTT	TATTTAAGT	ACCACCAIT	GAACCTTAAC	GAAGAAAAAA	60
ATCTTCAAGT	AGACCTAGAA	GAGAGTTT	AAAAACAAA	CAATGTAAGT	NAAGGATATT	120
TCTGAATCTT	AAAATTCATC	CCATGTGTGA	TCATAAACTC	ATAAAAAATA	TTTTAAGATG	180
TCGGAAAAGG	ATACCTTGAT	TAAATAAAAA	CACATCATGA	TATGTA AAAA	CTGTC AAGAT	240
TAANATTAA	TAGITTCATT	TATTTGTTAT	TTTATTTGTA	AGANATAGTG	ATGAACAAAG	300
A						301

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAAAAAATC	TTCAAGTAGA	CCTAGAAGAG	AGTTTTAAAA	AACAAAAACA	TGTAAGTAAA	60
GGATATTTCT	GAATCTTAAA	ATTTCATCCCA	TGTGTGATCA	TAAACTCATA	AAATAAATTT	120
TAAGATGTGC	GAAAAAGGATA	CTTTGATTAA	ATAAAACAC	TCATGGATAT	GTA AAAA CTG	180
TCAAGATTAA	AATTTAATAG	TTTCATTAT	TTGTTATTTT	ATTTGTAAG		229

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3043 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTAGAGAGGA	ACAATGGGGT	TATTCAGAGG	TTTTGTTTTT	CTCTAGTTC	TGTGCTGCT	60
GCACCAAGTCA	AATACTTCT	TCATTAAAGCT	GAATAATAAT	GGCTTTGAAG	ATATTGTGAT	120
TGTTATAGAT	CCTAGTGTGC	CAGAAGATGA	AAAAATAATT	GAACAAATAG	AGGATATGGT	180
GACTACAGCT	TCTACGTACC	TGTTTGAAGC	CACAGAAAAA	AGATTTTTTT	TCAAAAATGT	240
ATCTATATTA	ATTCCGTAGA	ATTGGAAGGA	AAATCCTCAG	TACAAAAGGC	CAAAAACATGA	300
AAACCATAAA	CATGCTGATG	TTATAGTTGC	ACCACCTACA	CTCCAGGTA	GAGATGAACC	360
ATACACCAAG	CAGTTCACAG	AATGTGGAGA	GAAAGGCGAA	TACATTCACT	TCACCCCTGA	420
CCTTCTACTT	GAAAAAAAAC	AAAATGAATA	TGGACCACCA	GGCAAACTGT	TTGTCCATGA	480
TGTGGGCTCAC	CTCCGGTGGG	GAGTGTTTGA	TGAGTACAA	GAAGATCAGC	CTTTCTACCG	540
TGCTAAGTCA	AAAAAAATCG	AAGCAACAAG	GTGTTCCGCA	GGTATCTCTG	GTAGAAAATAG	600
AGTTTATAAG	TGTC AAGGAG	GCAGCTGTCT	TAGTAGAGCA	TGCAGAAATT	ATTCTACAAC	660
AAAACTGTAT	GGAAAAGATT	GTCAATTCTT	TCCTGATAAA	GTACAAAACAG	AAAAAGCATC	720
CATAATGTTT	ATGCAAGAAT	TTGATTCTGT	TGTTGAATTT	TGTAACGAAA	AAACCCATAA	780
TCAAGAAGCT	CC AAGCTAC	AAACACATAA	GTGCAATTTT	AGAAGTACAT	GGGAGGTGAT	840
TAGCAATTCT	GAGGATTTTA	AAAAACACCAT	ACCCATGTGT	ACACCACCTC	CTCCACCTGT	900

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CTTCTCATTTG	CTGAAGATCA	GTCAAAGAAT	TGTTGTGCTTA	GTTCCTTGATA	AGTCTGGGAAG	960
CATGGGGGGT	AAGGACCGCC	TAAATCGAAT	GAATCAAGCA	GCAAAACATT	TCCCTGCTGCA	1020
GACTGTTGAA	AATGGATCTCT	GGGTGGGGAT	GGTTCACATT	GATAGTACTG	CCACTATTGTT	1080
AAATAAGCTA	ATCCAAATAA	AAAGCAGTGA	TGAAAGAAAC	ACACTCATGT	CAGGATTACC	1140
TACATATCCT	CTGGGAGGAA	CTTCCATCTG	CTCTGGAAAT	AAATATGTCAT	TTGAGGTGAT	1200
TGGAGAGCTA	CATTCCCAAC	TCGATGGATC	CGAAGTACTG	CTGCTGACTG	ATGGGGGAGGA	1260
TAACACTGCA	AGTTCTTTGT	TTGATGAAGT	GAACACAAAT	GGGGCCATTG	TTTCAATTTAT	1320
TGCTTTGGGA	AGAGCTGTGT	ATGAAGCAGT	AATAGAGATG	AGCAAGATAA	CAGGAGGAAG	1380
TCATTTTAT	GTTCCTAGAT	AAAGTCAGAA	CAATGGCCTC	ATTGATGCTT	TGGGCGCTCT	1440
TACATCAGGA	AATACGATC	TCTCCAGAA	GTCCCTCTAG	CTCGAAGCTT	AGCGATTAAAC	1500
ACTGAATAGT	AATGCTCGGA	TGAACGACAC	TGTCATAATT	GATAGTCAG	TGGGAAGAAG	1560
CACGTTCTTT	CTCATCACAT	GGAACAGTCT	CCCTCCCACT	ATTTCTCTCT	GGGATCCAG	1620
TGGAACAATA	ATGGAATAAT	TCACAGTGA	TGCAACTTCC	AAAATGGCTT	ATCTCAGTAT	1680
TCCAGGAAC	GCAAGGTGG	GCACCTGGGC	ATACAATCTT	CAAGCCAAAG	CGAACCCGAC	1740
AACATTAAC	ATTACAGTAA	CTTCTCGAC	AGCAAAATCT	TCTGTGCCTC	CAATCACAGT	1800
GAATGCTAAA	ATGAATAAGG	ACGTAAACAG	TTTCCCCAGC	CCAATGATTG	TTTACGCGAC	1860
AATCTTACAA	TAGATATGAT	CTGTTCTGG	AGCCAATGTG	ACTGCTTTCA	TTGAATCAC	1920
GAATGGACAT	ACAGAAGTTT	TGGAACTTT	GGATAATGTT	GCAGGCGCTG	ATTTCTTCAA	1980
GAATGATGGA	GTCTACTCCA	GGTATTTTAC	AGCATATACA	AAAAATGGCA	GATATAGTGT	2040
AAAAGTTCCG	GTCATGTCAG	GAGCAACAC	TGCCAGGCTA	AAATTACCGC	CTCCACTGAA	2100
TAGAGCCCGG	CACATACCCG	GCTGGGTAGT	GAACGGGGAA	ATTGAAGCAA	ACCCGCCAAG	2160
ACCTGAATTT	CTGAGAGATA	CTCAGACCAC	CTTTGGAGAT	TTCAGCCGAA	CAGCATTCGG	2220
AGGTGCTATT	TGTGATCTAC	AAGTCCCAAG	CCTTCCCTTG	CTTGACCAAT	ACCCACCAAG	2280
TCAATCACA	GAATCTGATG	CCACAGTTCA	TGAGGATAAG	ATTATTTCTA	CATGGACAGG	2340
ACGAGGAGAT	AACTTTGATG	TTGGAAGAAT	CTTGACCTAT	ATCATAGAA	TAAGTGCAGG	2400
TATTTCTTAT	CTAAGAGACA	GTTTTGATGA	TGCTCTTTCA	GTAATACTA	CTGATCTGTG	2460
ACCAAGAGAG	CCCAACTTCA	AGGAAGCTT	TGCAATTTAA	CCAGAAGAA	TCTCAGAAGA	2520
AAATGCAAC	CACATATTTA	TTGCCATTAA	AAGTATTAGT	AAAAGCAAT	TGACATCAAA	2580
AGTATCAAC	ATTGCACAAG	TAACCTTTGT	TATCCCTCAA	GCAAACTCTG	ATGACATTGA	2640
TCTCTACTCT	ACTCTCTACT	CTACTCTCTG	TAAAGTCAT	AATTTCTGGG	TTAATATTTC	2700
TACCGTGGTA	TTGCTCTGTG	TGGGCTCTGT	TGTAATTTGT	AACTTTTATT	TAAGTACCAC	2760
CATTGTGAAC	TTACGAGAAG	AAAAATCTTT	CAAGTAGACC	TAGAAGAGAT	TTTTAAAAAA	2820
CAAAAACAAT	TAGTCTCTGA	ATATTTCTGA	ATCTTAAAT	TCACTCCATG	TGTGATCAT	2880
AACCTCATAA	AATATTTTAT	AGATGTCGGA	AAAGGATACT	TTGATTAAT	AAAAACACTC	2940
ATGGATAGT	AAAAACTGTC	AAGATTAAAA	TTTATAGTT	TCATTTATTT	GTTATTTTAT	3000
TTGTAAGAAA	TAGTGATGAA	CAAAGATCCT	TTTTCTACT	GAT		3043

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCAAAATCTT	CTGTGCTTCC	AATCAGCTG	AATGCTAAAA	TGAATAAGGA	CGTAAACAGT	60
TTCCCCAGCC	CAATAGTGTG	TACGCGAGAA	ATTCTACAAG	GATATGTACC	TGTTCTTGGA	120
GCCAATGTGA	CTGCTTTTAT	TGAATCACAG	AATGGACATA	CAGAAGTTT	GGCACTTTTG	180
GATAATGTGT	CAGGCGCTGA	TCTTTTCAAG	AAATGCGAG	TCTACTCCAG	GTAATTTTAC	240
GCATATACAG	AAAAATGGCAG	ATATAGCTTA	AAAGTCCCGG	CTCATGGAGG	ACCAACCACT	300
GCCAGGCTAA	AATTAACGGCC	TCACCTGAAT	AGAGCCCGCT	ACATACCCAG	CTGGGTAGTG	360
AACGCGGAAA	TTGAAGCAAAA	CCCGCCAGGA	CTGCAAAATG	ATGAGGATAC	TCGACCAACC	420
TTGGAGAGAT	TCAGCCGGAAC	AGCATCCGGA	GTGTGCAATT	TGGTATACCA	AGTCCCAAGC	480
CTTCCCTTGC	CTGACCAATA	CCCACTCAAG	CMAATCACAG	ACCTTGATGC	CACAGTTTCA	540
GAGGAATAAG	TTATTTCTAC	ATGGACAGCA	CCAGGAGATA	ATTTTGATGT	TGGAAAAGTT	600
CACAGCTTCA	TGATTAAGAT	AAGTGCAAGT	ATTCTTGATC	TAAGAGAGAT	TTTTTGATGT	660
GCTCTTTAAG	TAAATATCTAC	TGATCTGTCA	CCAAAGGAGG	CCAACCTCAA	GGAAGGCTTT	720
CGATTAAAC	CAGAAAATAT	CTCAGAAGAA	ATGTCAACCC	ACATATTTAT	TGCCATTAAA	780
AGTATAGATA	AAAGCAATTT	GACATCAAAA	GTATCCAACA	TTGCAACAGT	AACCTTTGTT	840
ATCCCTCAAG	CAAACTCTGA	TGACATTGAT	CCTACTCTTA	CTCCTACTCC	TACTCTGTAT	900
AAAGTGCATA	ATTCTGAGAT	TAATATTCTT	ACGCTGGTAT	TGTCGTGTAT	TGGGTCTGTT	960
GTAATTTGTA	ACTTTATTTT	AGTACCACCC	ATTTGAACTT	TAACGAAGAA	AAAAATCTTC	1020

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AAGTAGACCT	AGAAGAGAGT	TTTAAAAAAC	AAAACAATGT	AAGTAAAGGA	TATTCTTGAA	1080
TCTTAAATTT	CATCCCATGT	GTGATCATAA	ACTCATAAAA	ATAATTTTAA	GATGTCGGAA	1140
AAGGATATCT	TGATTAATAA	AAAAACATCA	TGGATATGTA	AAAACTGTCA	AGATTAAAAAT	1200
TTAATAGTCT	CATTATTATT	TTATTATTAT	TGTAAGAAAT	AGTGATGAAC	AAAGATCCCT	1260
TTTCATACGT	ATACCTGGTT	GTATATTATT	TGATGCAACA	GTTCCTCTGA	ATGATATTTT	1320
AAATTCATC	AAGAATTTAA	AATCATCTAT	CTGAGTAGTC	AAAAACAAG	TAAAGGAGAG	1380
CAATAAACA	ACATTGGA					1399

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCAGGAATA	ACTAGAGAGG	AACAATGGGG	TTATTCAGAG	GTTTTGTTTT	CCTCTIAGTT	60
CTGTGCGCTG	TGCACCAAGT	AAATATCTCC	TTCAATTAAG	TGAATTAATA	TGGCTTTGAA	120
GATATTGTCA	TGTTTATAGA	TCTAGTGTG	CCAGAAGATG	AAAAAATAAT	TGAACAAATA	180
GAGGATATGG	TGACTACAGC	TTCTACGTAC	CTGTTTGAAG	CCACAGAAAA	AGAGTTTTTT	240
TTCAAAAATG	TATCTATATT	AATTCCTGAG	AATTGGAAAG	AAAACTCTCA	GTCACAAAAG	300
CCAAACATAT	AAAACCATAA	ACATGCTGAT	GTATATGTTG	CACCACTTAC	ATCTCCAGGT	360
AGAGATGAGC	CATACACCAA	CGAGTTCACA	GAATGTGGAG	AGAAAGGGGA	ATACATTTCAC	420
TTCAACCCCTG	ACCTTCTACT	TGAAAAAATA	CAAAATGAAAT	ATGGACCACC	AGGCAAACTG	480
TTTGTCCATG	AGTGGGCTCA	CTCCCGGTGG	GGAGTGTTTG	ATGAGTACAA	TGAGATCAGT	540
CCTTTCTACC	GTGCTAAGTC	AAAAAAAATC	GAAGCAACAA	GGGTGTCGCG	AGGTATCTCT	600
GGTAGAAATA	GAGTTTATAA	GTGTCAAGGA	GGCAGCTGTC	TTAGTAGAGC	ATGCAGAAAT	660
GATTCTACAA	CAAAACGTGA	TGGAAAAAGT	TGTCATTTCT	TTCTTGATAA	AGTACAAACA	720
GAAAAAGCAT	CCATAATGTT	TATGCAAGAT	ATTGATCTGT	TTGTGTAATT	TTGTAAACGA	780
AAAAACCCATA	ATCAAGAAGC	TCCAAGCCTA	CAAAACATAA	AGTGCATTTT	TAGAAGTACA	840
TGGGAGGTGA	TTAGCAATTC	TGAGGATTTT	AAAAACACCA	TACCCATGGT	GACACCACTT	900
CTCTCACCTG	TCTTCTCATT	GCTGAAGATC	AGTCAAAGAA	TTGTGTGCTT	AGTCTCTGAT	960
AAGTCTGGAA	GCAATGGGGG	TAAGGACCGC	CTAAATCGAA	TGATCTCAAG	AGCAAAACAT	1020
TTCTGCTGCG	AGACTGTGTA	AAATGGATCC	TGGGTGGGGA	TGTTCTCACT	TGATAGTACT	1080
GCCACTATTG	TAAATAAGCT	AATCCAAATA	AAAAGCAGTG	ATGAAAGAAA	CACACTCATG	1140
GCAGGATTAC	CTACATATCC	TCTGGGAGGA	ACTTCATCTC	GCTCTGGAAT	TATCATTGCA	1200
TTTCAGGTGA	TTGGAGAGCT	ACATTCCCAA	CTCGATGTAAT	CCGAAGTAAT	GCTGTGACTT	1260
GATGGGGGAG	ATACACTGCG	AGAGTCTGTG	ATTGATGAAG	TGAACAACTG	TGGGGCCATT	1320
GTTCATTGTT	TGCTTTGGG	AGAAGCTCTG	GATGAAGCAG	TAATAGAGAT	GAGCAAGATA	1380
ACAGGAGGAA	GTCACTTTTA	TGTTTCAGAT	GAAGCTCAGA	ACAAATGGCT	CATTGTGCTT	1440
TTTGGGGCTG	TATACATCAG	AAATACTGAT	CTCTCCCGAG	AGTCCCTTCA	GCTCGAAGAT	1500
AAGGGATTTA	CACGTGATAG	TAAATGCTGT	ATGAACGACA	CTGTCAATAA	TGATGTACAA	1560
GTGGGAAAGC	ACAGCTCTCT	TCTCATCACA	TGGAACAGTC	TGCTCCCGAG	TATTTCTCTC	1620
TGGGATCCCA	GTGACACAT	AATGGAAAAA	TTCAAGTGGG	ATGCAACTTC	CAAAATGGCC	1680
TATCTCAGTA	TTCCAGGAAC	TGCAAGGTGG	GGCACTTGGG	CATACAAATC	CTAAGGCCAA	1740
CGGAACCCAG	AAACATTTAA	TATTACAGTA	ACTTCTCGAG	CAGCAAACTT	TTCTGTGCTT	1800
CCAATCAGAC	TGAATGCTAA	AATGAATAAG	GACGTAAACA	GTTCCTCCAG	CCCAATGATT	1860
ATTACGCGAG	AAATCTCTCA	AGGATATGTA	CTGTCTCTTG	GAGCCAAATG	GACTGCTTTT	1920
ATTGAATCAC	AGAATGAGCA	TACAGAAATT	TTGGAACCTT	TGGAATATGG	TGCAGGCGCT	1980
GATTCCTTTA	AGAATGATGG	AGCTACTCTT	AGGTATTTTA	CAGCATATAC	AGAAATATGC	2040
AGATATAGCT	TAAAGTTTGG	GGCTCATGGA	GGAGCAAAACA	CTGCGAGGCT	AAAATATAGG	2100
CCTCCACTCA	ATAGAGCCGC	GTACATACCA	GGCTGGGTAG	TGAACGGGGA	AATTGAAAGG	2160
AACCCGCCAA	GACCTGAAAT	TGATGAGGAT	ACTCAGACCA	CCTTGAGAGA	TTTCACGCCA	2220
ACAGACTCCG	GAGGTGCAAT	TGTTGGTATCA	CAAGTCCCAA	GCCTTCCCTT	CGCTGACCAA	2280
TACCACCAAA	GTCAAAATCA	AGACCTTGAT	GCCACAGTTC	ATGAGGATAA	GATTATTTCT	2340
ACATGGACAG	CACCAAGAGA	TAATTTTGAT	GTGGAAGAACT	TTCAACATTC	TACATAAGA	2400
ATAAGTGCAA	GTATTCTTGA	TCTAAGAGAC	AGTTTTGATG	ATGCTCTTCA	AGTAAATACT	2460
ACTGATGATC	GACCAAAAGG	GGCCAACTCC	AAGGAAAGCT	TTGCAATTTA	ACCAAGAAAT	2520
ATTACAGAA	AAAATGCAAC	CCACATATTT	ATTGCCATTA	AAAGTATAGA	TAAAGCAAT	2580
TTCAGACATA	AAGTATCCAA	CATTGCACAA	GTAACCTTTG	TTATCCCTCA	AGCAAAATCT	2640
GATGACATTT	ATCCCTACTCT	TACTCTTACT	CCTACTCTGT	ATAAAGTACA	TAATTTCTGA	2700
TTTAATATTT	CTACGCTGGT	ATTGTCTGTG	ATTGGGTCTG	TTGTAATTTG	TAACTTTTAT	2760
TTAAGTACCA	CCATTGGAAC	CTTAACGAAG	AAAAAAATCT	TCAAGTAGAC	CTAGAAGAGA	2820

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GTTTTAAAA	ACAAAACAAT	GTAAGTAAAG	GATATTTCTG	AATCTTAAAA	TTCATCCCAT	2880
GTGTGATCAT	AAACTCATAA	AAATAATTTT	AAGATGTCGG	AAAAGGATAC	TTTGATTAAA	2940
TAAAAACACT	CATGGATATG	TAAAAACTGT	CAAGATTAAA	ATTTAATAGT	TTCATTTATT	3000
TGTTATTTTA	TTTGTAAGAA	ATAGTGATGA	ACAAAGATCC	TTTTTCATAC	TGATACCTGG	3060
TTGTATATTA	TTTGTATGCA	CAGTTTTCTG	AAATGATATT	TCAAATTGCA	TCAAGAAATT	3120
AAAATCATCT	ATCTGAGTAG	TCAAATACA	AGTAAAGGAG	AGCAAATAAA	CAACATTTGG	3180
A						3181

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATTAATTC	CGGTCGACG	AGTCACTAG	TCGCGGCCCG	CTCTAGAGGA	TCCAAGCTCG	60
GAATTCGG						68

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCGGATAAC	AATTTCACAC	AGGA	24
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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTAAAACGA	CGGCCAGT	18
------------	----------	----

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGCCAGGCT AAAATTACGG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCACAGACC TTGATGCCAC

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTGGTATTG TCTGTGATTG GSTC

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATCAGGATT TGCCTGAGGG

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TATTGGTCAG GCAAGGGAAG

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTGTTTGCTC TC CATGAGC

20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAAGTAGAAG GTCAGGGGTG

20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATAAGTGTCA AGGAGGCAGC

20

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCAGACTGTI CCATGTGATG

20

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGTACCTGT TCTTGAGGCC

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACGTACCTGT TTGAAGCCAC

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTAAGGACC GCCTAAATCG

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAAGTGAAC AAAGTGGGCG

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTATCCTCCC CATCAGTCAG

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCGATTTAGG CGGTCCTTAC

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGTGGCTTCA AACAGGTACG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGGTAAGGAC CGCCTAAATC GAATG

25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAGCCCCAAA AGCATCAATG AGG

23

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met	Gly	Leu	Phe	Arg	Gly	Phe	Val	Phe	Leu	Leu	Val	Leu	Cys	Leu	Leu
1				5				10					15		
His	Gln	Ser	Asn	Thr	Ser	Phe	Ile	Lys	Leu	Asn	Asn	Asn	Gly	Phe	Glu
			20					25					30		
Asp	Ile	Val	Ile	Val	Ile	Asp	Pro	Ser	Val	Pro	Glu	Asp	Glu	Lys	Ile
		35					40					45			
Ile	Glu	Gln	Ile	Glu	Asp	Met	Val	Thr	Thr	Ala	Ser	Thr	Tyr	Leu	Phe
		50				55					60				
Glu	Ala	Thr	Glu	Lys	Arg	Phe	Phe	Lys	Asn	Val	Ser	Ile	Leu	Ile	
65					70				75				80		
Pro	Glu	Asn	Trp	Lys	Glu	Asn	Pro	Gln	Tyr	Lys	Arg	Pro	Lys	His	Glu
			85					90					95		
Asn	His	Lys	His	Ala	Asp	Val	Ile	Val	Ala	Pro	Pro	Thr	Leu	Pro	Gly
			100					105					110		
Arg	Asp	Glu	Pro	Tyr	Thr	Lys	Gln	Phe	Thr	Glu	Cys	Gly	Glu	Lys	Gly
		115					120					125			
Glu	Tyr	Ile	His	Phe	Thr	Pro	Asp	Leu	Leu	Leu	Glu	Lys	Lys	Gln	Asn
		130					135				140				
Glu	Tyr	Gly	Pro	Pro	Gly	Lys	Leu	Phe	Val	His	Glu	Trp	Ala	His	Leu
145					150					155					160

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Arg	Trp	Gly	Val	Phe	Asp	Glu	Tyr	Asn	Glu	Asp	Gln	Pro	Phe	Tyr	Arg
				165					170					175	
Ala	Lys	Ser	Lys	Lys	Ile	Glu	Ala	Thr	Arg	Cys	Ser	Ala	Gly	Ile	Ser
			180					185					190		
Gly	Arg	Asn	Arg	Val	Tyr	Lys	Cys	Gln	Gly	Gly	Ser	Cys	Leu	Ser	Arg
		195					200					205			
Ala	Cys	Arg	Ile	Asp	Ser	Thr	Thr	Lys	Leu	Tyr	Gly	Lys	Asp	Cys	Gln
	210					215					220				
Phe	Phe	Pro	Asp	Lys	Val	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Met
225					230					235					240
Gln	Ser	Ile	Asp	Ser	Val	Val	Glu	Phe	Cys	Asn	Glu	Lys	Thr	His	Asn
				245					250					255	
Gln	Glu	Ala	Pro	Ser	Leu	Gln	Asn	Ile	Lys	Cys	Asn	Phe	Arg	Ser	Thr
			260					265					270		
Trp	Glu	Val	Ile	Ser	Asn	Ser	Glu	Asp	Phe	Lys	Asn	Thr	Ile	Pro	Met
		275					280					285			
Val	Thr	Pro	Pro	Pro	Pro	Pro	Val	Phe	Ser	Leu	Leu	Lys	Ile	Ser	Gln
	290					295					300				
Arg	Ile	Val	Cys	Leu	Val	Leu	Asp	Lys	Ser	Gly	Ser	Met	Gly	Gly	Lys
305					310					315					320
Asp	Arg	Leu	Asn	Arg	Met	Asn	Gln	Ala	Ala	Lys	His	Phe	Leu	Leu	Gln
			325					330						335	
Thr	Val	Glu	Asn	Gly	Ser	Trp	Val	Gly	Met	Val	His	Phe	Asp	Ser	Thr
		340						345					350		
Ala	Thr	Ile	Val	Asn	Lys	Leu	Ile	Gln	Ile	Lys	Ser	Ser	Asp	Glu	Arg
		355				360						365			
Asn	Thr	Leu	Met	Ala	Gly	Leu	Pro	Thr	Tyr	Pro	Leu	Gly	Gly	Thr	Ser
	370				375					380					
Ile	Cys	Ser	Gly	Ile	Lys	Tyr	Ala	Phe	Gln	Val	Ile	Gly	Glu	Leu	His
385					390				395						400
Ser	Gln	Leu	Asp	Gly	Ser	Glu	Val	Leu	Leu	Thr	Asp	Gly	Glu	Asp	
			405					410					415		
Asn	Thr	Ala	Ser	Ser	Cys	Ile	Asp	Glu	Val	Lys	Gln	Ser	Gly	Ala	Ile
		420					425						430		
Val	His	Phe	Ile	Ala	Leu	Gly	Arg	Ala	Ala	Asp	Glu	Ala	Val	Ile	Glu
	435						440				445				
Met	Ser	Lys	Ile	Thr	Gly	Gly	Ser	His	Phe	Tyr	Val	Ser	Asp	Glu	Ala
	450				455						460				
Gln	Asn	Asn	Gly	Leu	Ile	Asp	Ala	Phe	Gly	Ala	Leu	Thr	Ser	Gly	Asn
465				470					475						480
Thr	Asp	Leu	Ser	Gln	Lys	Ser	Leu	Gln	Leu	Glu	Ser	Lys	Gly	Leu	Thr
				485				490						495	
Leu	Asn	Ser	Asn	Ala	Trp	Met	Asn	Asp	Thr	Val	Ile	Ile	Asp	Ser	Thr
			500				505						510		
Val	Gly	Lys	Asp	Thr	Phe	Phe	Leu	Ile	Thr	Trp	Asn	Ser	Leu	Pro	Pro
		515					520					525			
Ser	Ile	Ser	Leu	Trp	Asp	Pro	Ser	Gly	Thr	Ile	Met	Glu	Asn	Phe	Thr
	530					535					540				
Val	Asp	Ala	Thr	Ser	Lys	Met	Ala	Tyr	Leu	Ser	Ile	Pro	Gly	Thr	Ala
545					550					555					560
Lys	Val	Gly	Thr	Trp	Ala	Tyr	Asn	Leu	Gln	Ala	Lys	Ala	Asn	Pro	Glu
				565				570						575	
Thr	Leu	Thr	Ile	Thr	Val	Thr	Ser	Arg	Ala	Ala	Asn	Ser	Ser	Val	Pro
			580					585					590		
Pro	Ile	Thr	Val	Asn	Ala	Lys	Met	Asn	Lys	Asp	Val	Asn	Ser	Phe	Pro
		595					600					605			
Ser	Pro	Met	Ile	Val	Tyr	Ala	Glu	Ile	Leu	Gln	Gly	Tyr	Val	Pro	Val
	610					615					620				
Leu	Gly	Ala	Asn	Val	Thr	Ala	Phe	Ile	Glu	Ser	Gln	Asn	Gly	His	Thr
625					630					635					640
Glu	Val	Leu	Glu	Leu	Leu	Asp	Asn	Gly	Ala	Gly	Ala	Asp	Ser	Phe	Lys
				645					650					655	
Asn	Asp	Gly	Val	Tyr	Ser	Arg	Tyr	Phe	Thr	Ala	Tyr	Thr	Glu	Asn	Gly
			660					665					670		
Arg	Tyr	Ser	Leu	Lys	Val	Arg	Ala	His	Gly	Gly	Ala	Asn	Thr	Ala	Arg
		675					680						685		

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Leu Lys Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp
690 695 700
Val Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp
705 710 715
Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser Gly
725 735
Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro Asp Gln
740 745 750
Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val His Glu Asp
755 760 765
Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn Phe Asp Val Gly
770 775 780
Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala Ser Ile Leu Asp Leu
785 790 795 800
Arg Asp Ser Phe Asp Asp Ala Leu Gln Val Asn Thr Thr Asp Leu Ser
805 810 815
Pro Lys Glu Ala Asn Ser Lys Glu Ser Phe Ala Phe Lys Pro Glu Asn
820 825 830
Ile Ser Glu Glu Asn Ala Thr His Ile Phe Ile Ala Ile Lys Ser Ile
835 840 845
Asp Lys Ser Asn Leu Thr Ser Lys Val Ser Asn Ile Ala Gln Val Thr
850 855 860
Leu Phe Ile Pro Gln Ala Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr
865 870 875 880
Pro Thr Pro Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser
885 890 895
Thr Leu Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile
900 905 910
Leu Ser Thr Thr Ile
915

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ala Asn Ser Ser Val Pro Pro Ile Thr Val Asn Ala Lys Met Asn Lys
1 5 10 15
Asp Val Asn Ser Phe
20

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys Asn Asp Gly Val Tyr Ser
1 5 10 15
Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly Arg Tyr Ser Leu Lys
20 25 30

(2) INFORMATION FOR SEQ ID NO:44:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg Leu Lys Leu Arg Pro
1 5 10 15
Pro Leu Asn Arg Ala Ala Tyr Ile
20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Leu Pro Leu Pro Asp Gln Tyr Pro Pro Ser Gln Ile Thr Asp Leu
1 5 10 15
Asp Ala Thr Val His Glu Asp Lys Ile Ile Leu Thr Trp Thr Ala Pro
20 25 30
Gly Asp Asn Phe Asp Val Gly Lys
35 40

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Tyr Asn Glu Asp Gln Pro Phe Tyr Arg Ala Lys Ser Lys Lys Ile Glu
1 5 10 15
Ala Thr Arg Cys
20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

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Leu Ser Arg Ala Cys Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys
 1 5 10 15
 Asp Cys Gln Phe Phe Pro Asp Lys
 20

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Lys Ser Ser Asp Glu Arg Asn Thr Leu Met Ala Gly Leu Pro Thr Tyr
 1 5 10 15
 Pro Leu Gly Gly
 20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Glu Ile Asp Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp Tyr Lys Asp Asp Asp Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

10025167.121901

Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Met	His	Thr	Glu	His
1				5					10					15	
His	His	His	His	His											
				20											

10025167.121901